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WLKTRQ

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C.J.,


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BASE COUNT    91 a      83 c      94 g      89 t

Query Match          4.0%; Score 13; DB 2; Length 357;
Best Local Similarity 65.5%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy      22 GATACCGGAGCGGCCACCACAGCGGGCCC 50
        ||||| ||| ||| | | || |||||
Db       141 GATTATCCAGGCCCGCAGAGACAACGCGCC 113

RESULT 5
AY072430/c
LOCUS     AY072430             666 bp      mRNA      linear      PLN 21-JAN-2002
DEFINITION Arabidopsis thaliana ring-box protein - like (At5g20570) mRNA,
complete cds.
ACCESSION AY072430
VERSION   AY072430.1 GI:18252990
KEYWORDS  FTI CDNA.
SOURCE    Arabidopsis thaliana.
ORGANISM  Arabidopsis thaliana.
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi-.
1 (bases 1 to 666)
AUTHORS   Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
Shinozaki,K., Eckert,J., Theologis,A. and Davis,R.W.
TITLE     Submitted (02-JAN-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
JOURNAL
COMMENT   e-mail for correspondence: arabsequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
Yamada,K., Eckert,J., Theologis,A. and Davis,R.W.

Nguyen,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PIs.

FEATURES
Source
Location/Organisms
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1..666
/gene="At5g20570"
88..444

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BASE COUNT	181 a	137 c	149 g	199 t
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Oy	22	GATACCCCGAGGCGCACCAACAGCGGCCG	50	
Db	228	GATATCCACAGCCCGACAGCAGCAGCCCC	200	
RESULT 6	SCYOYL134C	1255 bp	DNA	linear
LOCUS	S.cerevisiae chromosome XV reading frame ORF YOL134c.			PLN 11-AUG-1997
DEFINITION	Z74876.Y13140			
ACCESSION	Z74876.1			GI:1420022
VERSION				
KEYWORDS				
SOURCE	Saccharomyces cerevisiae.			
ORGANISM	Saccharomyces cerevisiae			
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. 1 (bases 1 to 1255) Alino,J., Casamuyor,A., Gamio,F.J., Gancedo,C., Lafuente,M.J., Aldea,M., Casas,C. and Herrero,E. Unpublished MIPS 2 (bases 1 to 1255)			
JOURNAL	Direct Submission			
AUTHORS	Submitted (04-JUL-1996) data collected by MIPS on behalf of the European yeast chromosome XV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.emblnet.org			
TITLE	Location/Qualifiers			
JOURNAL	1..1255			
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BASE COUNT	419 a	209 c	249 g	378 t
Query Match	Similarity	4.0%; Score 13;	DB 3; Length 1255;	
Best Local	Similarity	52.8%; Pred. No. 3;		
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Job time : 0.001 secs

0.001